

GENETIC VARIABILITY AND TRAIT ASSOCIATION ANALYSIS IN OKRA (*Abelmoschus esculentus* L. MOENCH)

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Association among different traits of 25 okra genotypes was ascertained to understand the direct and indirect contributions of plant traits with pod yield per plant which may help to develop high yielding okra varieties. The 25 genotypes of okra were sown in a field using randomized complete block design with three replications during the summer season 2014. The data for fruit yield, first flowering node, days to 50% flowering, number of pods per plant, plant height, number of internode, node(s) producing fruit on the main stem, stem diameter, number of seeds per pod, 100-seed weight, pod length at maturity, pods weight per plant and yield per plant were recorded and statistically analyzed for estimating genetic variability, direct and indirect effects of these characters on pod yield. All traits showed significant association with pod yield except first flowering node and stem diameter at maturity. Path analysis revealed that pod weight per plant, number of pods per plant, plant height at maturity and 100 seed weight contributed largely to okra pod yield and maximum emphasis would be given to these traits for selection focused at development of high yielding okra varieties.

Keywords: Variability, Trait, Pods, Maturity, Seed weight, Okra, Path Analysis

INTRODUCTION

Vegetables are normally consumed fresh and contain various minerals, vitamins, carbohydrates, proteins, medicinal and therapeutic agents, which are essential for healthy living (Adiger *et al.*, 2011; Gangashetty *et al.*, 2010). During the recent years, the interest in vegetables production throughout the world especially in developing countries such as Pakistan has increased rapidly due to its importance in the diet of the people and economy of the country. Okra belongs to Malvaceae family having somatic chromosome number 130. Its exact center of origin is still unknown but center of diversity is found in tropical Africa and subtropical Asia (Purseglove, 1974). It is an oldest crop that is grown for food and is well adapted to warm climates in the world. It belongs to often cross pollinated group, cross pollination ranging from 8.75 to 9.61% and has no photoperiodic effect on flowering as a day neutral plant.

Okra is famous for its immature tender pods that are rich in calcium, iron, and vitamin C (Pal *et al.*, 1952). Its mucilage is used as food additive and to cure gastric and inflammatory diseases. (Lengsfeld *et al.*, 2007). It contains anti-oxidant and anti-diabetic compounds that make it medically important and it is also used as plasma replacement (Kumar *et al.*, 2010). Okra seed also contains 25% protein and 14% edible oil content (NARP, 1993). It has many local names in different parts of the world such as lady's finger, gumbo, guino-gombo, guibeiro and bhindi.

Okra is commercially grown due to its medicinal and industrial properties and has high economic value because of greater export potential. India and Nigeria are two main producing countries but India is leading due to national consumer preferences and increased per unit area yields. Pakistan is producing 113,200 thousand tons out of total area of 13.9 ha while it is grown on total area of 1104 thousand ha with total production of 8.6 m tons in world (MINFAL, 2013). Favorable climatic conditions are available in Pakistan for okra production but average yield per unit area is not enough (Amjad *et al.*, 2001).

The objective here is to study the morphological and genetic variability for different economic characters in a set of 25 Okra genotypes considering that such information would help in selecting genotypes and planning effective breeding programmed for improvement of the crop. The genetic correlation considerably affects the process between different traits. The genetic correlation and heritability estimates provide extra information for the plant breeder to affect the selection process (Falconer and Mackay, 1996).

MATERIALS AND METHODS

The experimental material was planted under natural conditions in randomized complete block design (RCBD) with three replications comprising 24 accessions and one commercial variety (Sabz pari) in July 2014. The distance between plants and rows was maintained 30 and 60 cm,

respectively. Uniform cultural practices were carried out throughout growing season for good crop stand. Five random plants from each replication were selected for recording of data. Analysis of variance was carried out using the methods of Steel *et al.*, (1997). Genotypic and phenotypic correlation coefficient of variation were calculated according to the formula given by Kwon and Torrie (1964). Phenotypic and genotypic coefficients of variation will be estimated following Burton (1952).

All the analyses were performed using a program written and connected to MS Excel software.

Coefficient of variation: The phenotypic and genotypic coefficients of variation were calculated by the formula

GCV = Genotypic coefficient of variation (%)

$$GCV = \frac{\sqrt{\frac{\sigma_g^2}{\bar{X}}}}{\bar{X}} \times 100$$

PCV = Phenotypic coefficient of variation (%)

$$PCV = \frac{\sqrt{\frac{\sigma_p^2}{\bar{X}}}}{\bar{X}} \times 100$$

Where, \bar{X} = Grand mean of the trait, σ_p^2 = Phenotypic variance, σ_g^2 = Genotypic variance

Correlation Analysis: Phenotypic (r_p) and genotypic (r_g) correlation coefficient was calculated as outlined by Kwon and Torrie (1964).

$$r_p = \frac{M_{ij}}{\sqrt{(M_{ii})(M_{jj})}}$$

Where, M_{ij} = the mean product of genotypes for the i th and j th traits, M_{ii} and M_{jj} = Variety mean squares for i th and j th traits, respectively. r_p = the estimate of phenotypic correlation coefficient

$$r_g = \frac{Cov_{gij}}{\sqrt{(Var_{gi})(Var_{gj})}}$$

Where, r_g = Genotypic correlation coefficient, Cov_{gij} = Genotypic covariance of i th and j th traits

Var_{gi} = Genotypic variance of i th traits, Var_{gj} = Genotypic variance of j th traits, Genetic advance (GA) was calculated by the following formula

$$GA = \sigma_p \times h^2 \times i$$

Where, h^2 = Estimate of broad sense heritability, σ_p = The phenotypic standard deviation, i = Constant value (1.755) that reflects selection intensity (10%)

RESULTS AND DISCUSSIONS

Correlation is the tendency of relationship of two variables in a definite manner. In this relationship, it is customary to consider one variable as independent and the other as dependent. The main genetic cause of such correlation is pleiotropy which refers to diverse effects of a gene. If the relationship between two traits (whether positive or negative)

remains the same in the parental population as well as segregating populations, it means the association is due to pleiotropy. If it change in the segregating population, it is most likely due to linkage between two genes which had broken in the segregating population resulting in recombination between such genes. The pleiotropy or linkage involves two desirable character or one desirable and one unwanted trait. The first situation enhances the genetic improvement, whereas second hinders the progress.

Correlation analysis between yield and other various quantitative traits is the logical step in making sense about the contribution of these traits to grain yield. Phenotypic and genotypic correlation coefficients were estimated among all possible combinations of 12 different characters and are presented in Table 1. The observations regarding the association of various traits are explained separately as under. In general, the genotypic correlation coefficients were larger as compared to their respective phenotypic correlation coefficients. This shows greater involvement of genotypic factors in the development of relationship.

Correlation between first flowering node and other traits:

Table 1 showed that the correlation between first flowering node with number of seed per pod and nodes producing fruit on main stem were found negative and non-significant on genotypic and phenotypic level. First flowering node was observed positive and highly important with days to 50% flowering, plant height at maturity and number of internode per plant on both genotypic and phenotypic levels which revealed that smaller the number of first flowering node was shorten the days to 50% flowering, enhanced the plant height and had increased the internode per plant. First flowering node had negative and highly important correlation with pod length, number of seed per pod, pod width on genotypic and phenotypic levels. This study revealed that higher the value of first flowering there was a decrease in above mentioned negatively yield contributing traits. First flowering node was observed positive but significant on genotypic level correlated with pod weight per plant. First flowering node was detected positive but non-significantly correlated with pod yield per plant. Similar results had been observed by Jaiprakashnarayan and Mulge (2004) and Saryam *et al.*, (2015).

Correlation analysis of days to 50% flowering and other traits:

Table 2 indicates that the correlation between days to 50% flowering was depicted positive and non-significant with plant height at maturity, number of internode per plant, 100 seed weight and pod weight per plant on both genotypic and phenotypic levels. Days to 50% flowering had harmful and highly significant association with number of pods per plant, nodes producing fruit on main stem, stem diameter at maturity, number of seed per pod, pod length at maturity on genotypic and phenotypic levels. This study revealed that there was a decrease in above mentioned negatively yield contributing traits with an increase in days to 50% flowering. Correlation was found negative and highly important between

days to 50% flowering and pod yield per plant which showed that as the days to 50% flowering increases there was a decrease in pod yield per plant. Similar results had discussed by Mishra and Singh (1985); Hazare and Basu (2000); Dhankar and Dhankar (2002); Das *et al.*, (2012).

Correlation analysis of pods per plant and other traits: Table 1 depicted that number of pods/plant have undesirable but imperative correlation with days to 50 percent of flowering on phenotypic and genotypic levels. No. of pods/plant exhibited desirable but non-significant relation with plant height at maturity, no. of internodes/plant, no. of seed/pod, 100-seed weight and pod weight/plant on genotypic and phenotypic levels. Vastly significant and desirable relation had observed between number of pods/plant with nodes producing fruit on main stem, stem diameter at maturity, pod length at maturity on phenotypic and genotypic levels. Positive but highly momentous character association was found among no. of pods/plant with pod yield/plant indicating a high pod yield/plant with more no. of pods/plant. Ajmal *et al.*, (1979), Shukla (1990), Yadav (1996), Paiva *et al.*, (1998), Hazara and Basu (2000), Dhankar and Dhankar (2002), Singh *et al.*, (2006) and Das *et al.*, (2012) had reported the similar results.

Correlation between plant height and other traits: The results presented in Table 2 revealed that height of plant at maturity had highly significant correlation but positive effect with number of internodes per plant and nodes producing fruit on main stem on both phenotypic and genotypic levels. This indicated that more was the plant height more had been the number of internodes and nodes producing fruit on main stem. Plant height was observed positively and significantly correlated with stem width at maturity on genotypic and phenotypic levels. Plant height showed negative but non-significant correlation with pod length at maturity and also with number of seed per pod on and phenotypic and phenotypic levels. Non-significant but positive correlation was observed among 100 seed weight, pod weight per plant. Plant height showed non-significant positive correlation with pod yield per plant on genotypic level and positive significant correlation on phenotypic level. Result was same as figured out by Mishra and Singh (1985), Sood *et al.* (1995), Rajani and Manju (1997), Paiva *et al.* (1998), Dhall *et al.* (2001), Dhankar and Dhankar (2002), Niranjana and Mishra (2003) and Das *et al.* (2012).

Correlation analysis of internode per plant and other traits: Analyzed data presented in Table 2 showed that number of internodes per plant had non-significant but positive correlation with days to 50% flowering, nodes producing fruits on main stem, number of pods per plant, stem diameter at maturity and 100 seed weight on phenotypic and genotypic levels. Number of internode per plant showed positive and highly significant correlation with first flowering node, plant height at maturity and pod weight per plant. A highly significant and negative association had observed between pod length at maturity and number of internode per plant with

number of seed per pod on phenotypic and genotypic levels. Positive but significant character linkage found between numbers of inter node per plant with pod yield per plant indicate that as number of internodes increases will increase the pod yield per plant. Shukla (1990) Sood *et al.*, (1995) Rajani and Manju (1997) Kamal *et al.*, (2003) Bendale *et al.*, (2003) Balakrishnan and Sreenivasan (2010) had worked out the similar inferences.

Correlation between Nodes producing fruits on main stem and other trait: Table 2 revealed that nodes producing fruits on main stem had highly significant and positive correlation with plant height at maturity, number of pods per plant, 100 seed weight and pod length at maturity, stem diameter at maturity, on genotypic and phenotypic levels. Nodes producing fruit on main stem showed highly significant and negative correlation with days to 50% flowering on genotypic level and also negative significant relationship with first flowering node and number of seed per pod on phenotypic and genotypic levels. Nodes producing fruits on main stem showed non-significant and positive correlation with pod weight per plant and pod yield per plant, number of internode per plant on both phenotypic and genotypic levels on genotypic and phenotypic levels. Results were matched with findings of Paiva *et al.* (1998) Jaiprakashnarayan and Mulge (2004) Das *et al.*, (2012).

Correlation between stem diameter at maturity and other traits: It was revealed from Table 2, that stem diameter at maturity had highly significant but positive association with nodes producing fruit on main stem, number of pods per plant and pod length at maturity on genotypic and phenotypic levels. Stem diameter at maturity exhibited significant but positive association with plant height at maturity on genotypic and phenotypic level. With days to 50% flowering, stem diameter at maturity showed negative and highly significant correlation. Stem diameter at maturity had negative significant correlation with 100-seed weight on genotypic level but non-significant on phenotypic level which showed that 100 seed weight was found decreased as increase in stem diameter governed by genetic control. Stem diameter revealed positive but non-significant correlation with first flowering node, number of seed per pod, number of internode per plant, pod weight per plant and pod yield per plant. Similar results had been discussed by Das *et al.* (2012) and Saryam *et al.*, (2015).

Correlation between pod length and other traits: Results presented in Table 2 revealed that pod length had negative but highly significant relationship with days to 50% flowering on phenotypic and genotypic levels. Pod length showed negative but significant but relationship with number of internode per plant on phenotypic and genotypic level. Pod length had non-significant and negative correlation with plant height at maturity and also with 100 seed weight. Highly significant and positive relationship were observed with number of pods per plant, stem diameter at maturity, nodes producing fruit on

main stem, number of seed per pod and pod weight per plant. Pod length showed positive significant correlation with pod yield per plant at genotypic level but non-significant at phenotypic level which means that pod length was increased, there had been more pod yield per plant. Above stated results were also discussed by Shukla (1990) Sood *et al.*, (1995) Rajani and Manju (1997) Singh and Singh (2006) Bendale *et al.*, (2003) Niranjana and Mishra (2003) Singh *et al.*, (2006)

Correlation between pods weight per plant and other traits: Table 2 showed that pods weight per plant revealed significant and positive correlation with first flowering node on genotypic level only while there was non-significant relationship found at phenotypic level. Pods weight per plant was found positive and non-significantly associated with days to 50% flowering, plant height at maturity, number of pods per plant, nodes producing fruit on main stem, stem diameter at maturity, number of seed per pod and 100 seed weight. Pods weight per plant revealed significant positive correlation with pod yield per plant on genotypic level only while non-significant at phenotypic levels. Previous studies by Mishra and Singh (1985), Dhali *et al.* (2001), Singh and Singh (2006), Bendale *et al.* (2003), Niranjana and Mishra (2003), Singh *et al.* (2006), Patro and Sankar (2006) had confirmed the above stated results.

Correlation between pod yield per plant and other traits: A study of Table 2 revealed that pod yield per plant had negative but highly significant relationship with days to 50% flowering and 100 seed weight on both phenotypic and genotypic level. A highly significant but positive relationship was found between pod yield per plant with number of pods per plant and pods weight per plant on phenotypic and genotypic level. A positive significant inter-relationship was observed between pod yields per plant with number of internode per plant. Plant height at maturity and pod length at maturity were found considerably correlated with pod yield per plant on phenotypic level while non-significant on genotypic level. Correlation was found positive but non-significant between pod yield per plant and first flowering node, nodes producing fruit on main stem and stem diameter at maturity on genotypic and phenotypic levels.

Conclusion: Interrelationship among twelve different traits of 25 Okra genotypes was ascertained to understand the direct and indirect contributions of plant traits under observation to yield of Okra fruit per plant which may help to develop high yielding Okra varieties, that is ultimate objective of breeding programs. Genetic differences among the genotypes revealed by analysis of variance for first flowering node, days to 50% flowering, number of pods per plant, plant height, number of internode, node(s) producing fruit on the main stem, stem diameter, number of seeds per pod, 100-seed weight, pod length at maturity, pods weight per plant and yield per plant were highly significant. The path coefficients analysis was conducted to understand the role of each character to the fruit

yield per plant. Investigation regarding path coefficient showed that pod yield per plant and pod weight per plant had full direct influence on the yield of pod. The first flowering node, days to 50% flowering, nodes producing fruit on main stem, number of seed per pod and pod length at maturity had negative direct effects on the yield of pod of each plant. Nature of association among different pairs of characters were revealed by genetic correlation. It was found that the GCV were invariably inferior to their corresponding PCV mainly due to the environmental effect on the character expression. It was found that genotype PB-Okra-8 had a better yield performance as compared to other genotypes. Number of seed per pod, plant height at maturity, stem diameter at maturity and days to 50% flowering showed maximum heritability respectively which showed that selection could be more nominal for the genetic enhancement.

In conclusion, all the above facts divulged clearly that pod weight per plant, number of pods per plant, plant height at maturity and 100 seed weight are the characters found to be contributed largely to Okra fruit yield and maximum emphasis should be given to these traits during selection procedure focused at development of future high yielding Okra varieties.

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